

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 23, 2003, 13:00:00 ; Search time 22 Seconds
(without alignments)
2543.192 Million cell updates/sec

Title: US-09-635-949-34

Perfect score: 3289

Sequence: 1 MDELALIVVSSLYIQAAAF.....TGKLGIDVDSIKKKGHCSEER 582

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1066.5	32.4	558	2 T17324	hypothetical prote
2	406.5	12.4	2871	2 A55567	fibrillin 1 - bovi
3	402	12.2	1221	2 A49457	fibrillin-2 precurs
4	398.5	12.1	2871	2 A55624	fibrillin-1 precur
5	397.5	12.1	2918	2 A54105	fibrillin-2 precur
6	397	12.1	2907	2 A57278	fibrillin-1 precur
7	395.5	12.0	3002	2 A47221	fibrillin-2 precurs
8	381.5	11.6	1184	2 A55184	MEGF6 protein - ra
9	375.5	11.4	1574	2 T13954	hypothetical prote
10	357	10.9	1620	2 T27283	hypothetical prote
11	346	10.5	3507	2 T34513	fibrulin 1 precurs
12	340	10.3	683	2 C36346	fibrulin 1, splice
13	338	10.3	601	2 B36346	fibrulin, splice fo
14	334.5	10.2	685	2 S78040	fibrulin, splice fo
15	332	10.1	705	2 S34968	fibrulin-ID precurs
16	327	9.9	589	2 T43210	fibrulin, splice fo
17	327	9.9	589	2 T42760	hypothetical prote
18	327	9.9	741	2 T46488	fibrulin 1, splice
19	325	9.9	712	2 T42990	hypothetical prote
20	324.5	9.9	798	2 T2793	hypothetical prote
21	315.5	9.6	2555	2 A40043	notch protein homo
22	310.5	9.4	2524	2 A35844	Notch-1 protein - Af
23	308	9.4	2531	2 A46019	Notch-1 protein -
24	307	9.3	1247	1 MHUND	nidogen precursor
25	304	9.2	1820	2 A55494	latent transformin
26	301	9.2	493	2 JC5621	epidermal growth f
27	297	9.0	2531	2 S18188	notch protein homo
28	296	9.0	1712	2 A38261	masking protein pr
29	295.5	9.0	1394	2 A35626	transforming growt

RESULT 1

T17324

hypothetical protein DKFZp564P2063.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17324

R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18727

A:Accession: T17324

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-558 <DUE>

A:Cross-references: EMBL:AL117610

A:Experimental source: fetal brain; clone DKFZp564P2063

C:Genetics:

A:Note: DKFZp564P2063.1

Query Match

Best Local Similarity 32.4% ; Score 1066.5 ; DB 2: Length 558 ;

Matches 214 ; Conservative 95 ; Mismatches 175 ; Indels 87 ; Gaps 15 ;

Qy	34	GICRYGGRIDCCGWARSGCQCQPPYVIRQRIARIRQQLKAVCQPRCKHGECIGPNKCK	93
Db	44	GVCHYGTKLACCYGWRNRSGVCE-----ATCEPGCKFGECVGNPKCR	86
Qy	94	CHPGYAGTCTQVLFNFCGLKPRPCCKHRCMNITYGSYKCYCLNGYMLMPDSCSSALTC	153
Db	87	CLPGYTGKTCSDVNECGMKPRPCQRCVNTGHSYKCYCLSGHMLMPDTCVYSKTCAM	146
Qy	154	NCQYSCDVMKQIRQCQPSGLQLAPDGRCTVDVDECATGRASCPRRQCVNTGYSYCK	213
Db	147	NCQYSCDTEHGPQCICPSSGIRLAPNCRDCLIDECASGKVICYNNKRCVNTGYSYCK	206
Qy	214	CHKGFDLMYIGCKYQCHDIDECISGQYQCSSFARCYNNVRSYKCKKPGYQDGLTCVY	273
Db	207	CHIGFELQYISGRVDCIDINECTMSHTSSHHANCFNTQGSFKCKCKQYKGNGLRCSAI	266
Qy	274	PKVMIERPSPHVPKNGNTILKGDGTNNNMIPOVGSWPPKTPYIPPIINRPTSKPIT	333
Db	267	PENSVK-----EVLRAPGTI-----KDRIKLLAHKNSMKKA	299
Qy	334	R---PTPKPTPIPPPPPPPLTELRTPLPPTTPERTTGLTTTAPAASTPPG-----	383
Db	300	KIKVTPPTPTPTP-----KVMIQPNVE-----GI---VSRGSGSGKKGKNGEK	343
Qy	384	---GITVDNRVQ-----TDPKPRGDYFIPROPSNDLFEIPEIFERGVSADEAKDDPCV	434
Db	344	MKEGLEDEKREKALKNDIEERSLRGDVFFPKVNEAGEFGLLYVRKALTSKLEHKDINI	403
Qy	435	LVHSGNDPHGLCGWTREKNDLHWPEPT-RDPAGCGYILTVSAAKAPGGKAANLVLPIGLRI	493

ALIGNMENTS

30	295	9.0	387	2	138449	extracellular prot
31	293.5	8.9	2321	2	S78549	notch3 protein - h
32	290.5	8.8	1964	2	T09059	notch4 - mouse
33	288	8.8	1106	2	T18739	hypothetical prote
34	287	8.7	1245	1	MMNSND	nidogen precursor
35	286	8.7	2437	2	S42612	transmembrane prot
36	285.5	8.7	810	2	T10756	Nel-homolog protei
37	285.5	8.7	1376	2	G00043	osteonidogen - hum
38	283	8.6	1251	2	A57293	latent transformin
39	281	8.5	2318	2	S45306	notch 3 protein -
40	280.5	8.5	728	2	I50719	c-Delta-1 - chicke
41	279.5	8.5	2703	1	A24420	notch protein - fr
42	278	8.5	1220	2	A56136	jagged protein pre
43	275	8.4	577	2	A60501	thrombomodulin pre
44	273.5	8.3	886	2	A57172	probable hormone r
45	272.5	8.3	356	2	A25918	thrombomodulin - b

Db 404 SV-DCSFNHGICDMKQURDEHDFMNDADRENAIGPYMAVPAALAGHKKDIGRIKLLLPDILQ 462
 QY 494 HSGDLGLSFRHKVIGLSGTLOWEVKUGAAGALWGRNGHIG--WRQTQITL-RGAD-I 549
 Db 463 PQSNFCSLDYRLAGDKVGLRVEK--NSNNALAEKTTSEDEKKWTKGIQLYQGTDAT 520
 QY 550 KSVVPKGEKRRKRGHTGIGLIDVSLKKGHCSF 580
 Db 521 KSIIFVAERKGGKTGELAVDGVLLVSLGLCPD 551

RESULT 2
 A:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
 C:Accession: A55567
 R:Patra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Myers, P.H.
 Genomics 23, 480-485, 1994
 A:Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to
 A:Reference number: A55567; MUID:95137597; PMID:7835900
 A:Accession: A55567
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2871 <TILL>
 A:Cross-references: GR:128748, NID:9508427; PIDN:AAA74122.1; PID:9508428
 C:Superfamily: fibrillin 1; EGF homology
 F:1201-1236/Domain: EGF homology <EGF>

Query Match 12.4%; Score 406.5; DB 2; Length 2871;
 Best local similarity 32.0%; Pred. No. 8.5e-15;
 Matches 105; Conservative 32; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRVG-----GRIDCGWQWARGSQGCPFYVLRRIARI-----RCOLKAVQCPKCKIG 84
 Db 1123 LCRGGVCLNTEGYSRC-----KCPYHQIAINISACIDINNECELSA-----HICPHG 1169
 QY 85 EC-----IGPNKCKCHPGYAGKT-----CIQVLNEGLKPRCKHRCMNTYGSYKCYCLNGYM 137
 Db 1170 RCYNLIGKYCACNPGYHSTPDLFLCVDI-DEGSIHNGGCTCTNSGSEYSCOPGFA 1228
 QY 138 LMPD-GSCSSALTC--SMANCOYG-CDVVKGQIRKCCQPSGIGLADPGRCTCVW-----187
 Db 1229 LMPDQRSCDTIDECEDNPNICDGGCTNIPGKYKCLC-YDGFMASSDMKTCVDVNSCDLN 1287
 QY 188 -----DECATGRASCPREFRCQCVNTEGYSYI 211
 Db 1288 PNIICLSCTCHTKGSPICHCMDGYSCKKGTCTDINKEEIGAHNCDRAVCINTASSPK 1347
 QY 212 CKCHKGHDLIMYIGKGYOCHDIDECISLGOYCCSFARCYNVKSGYKCKKPGYCGDGLTCV 271
 Db 1348 CSCSPG---WIGDGKICKTDLDECSNCTUMCSQADCKNTMGSYRCLCKEYGTGDTCT 1403
 QY 272 YIPKVMIEPSCPIHVPKGNCTILKGDIG 299
 Db 1404 DLD-----ECSENLNL-CGNGCCLNAPCG 1426

RESULT 3
 A:Species: Mus musculus (house mouse)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 02-Aug-2002
 C:Accession: A49457
 R:Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.
 J. Cell Biol. 123, 1269-1277, 1993
 A:Title: Structure and expression of fibrulin-2, a novel extracellular matrix protein with
 A:Reference number: A49457; MUID:94064787; PMID:8245130
 A:Accession: A49457
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1221 <PAN>
 A:Cross-references: GR:X75285; NID:9437046; PIDN:CAA53040.1; PID:9437047

Db 404 SV-DCSFNHGICDMKQURDEHDFMNDADRENAIGPYMAVPAALAGHKKDIGRIKLLLPDILQ 462
 QY 494 HSGDLGLSFRHKVIGLSGTLOWEVKUGAAGALWGRNGHIG--WRQTQITL-RGAD-I 549
 Db 463 PQSNFCSLDYRLAGDKVGLRVEK--NSNNALAEKTTSEDEKKWTKGIQLYQGTDAT 520
 QY 550 KSVVPKGEKRRKRGHTGIGLIDVSLKKGHCSF 580
 Db 521 KSIIFVAERKGGKTGELAVDGVLLVSLGLCPD 551

Query Match 12.2%; Score 402; DB 2; Length 1221;
 Best local similarity 36.6%; Pred. No. 7.1e-15;
 Matches 93; Conservative 29; Mismatches 92; Indels 40; Gaps 14;

QY 80 RCKIGE-CI---GPNKCKCHPGYA---GKTCIOVLNEGLKPRCKHRCMNTYGSYK 130
 Db 905 RCGRGOLCYNLPGSYKCKCKPGQFQFATQFCTDV-NRWSPSGHICQHTENTETSYRC 963
 QY 131 YCINLYMIMPDS-CSSALTCSSMANCOYGCDVVKGQIRKCCQPSGIGLADPGRCTCVW 189
 Db 964 SCANGFLAADCCKICEDVNECETBRCSECCANTYGSYCYC-RCGYOLAEKGLTCTDDE 1022
 QY 190 CATGRASCPREFRCQCVNTEGYSYICKC-HKGFDMYIGKGYOCHDIDECISLGOYCCSFAR 248
 Db 1023 CAQAGCIICTFE-CVNVPGSYCACPEGQYTMNANG-RSCCKIDDECALGTHNCSSEATC 1079
 QY 249 YNVGSGYK---CKEGY-----QSDGLTCVYIPKVMIEPSC-----PIH 285
 Db 1080 HNIQGSFCLRFCDPNVYVKSQIKCERPTCDITFCQTSIPARITHYGLNFVGLLVIAH 1119
 QY 286 VPK-GNCTILKGIPT 298
 Db 1140 IFRIGPAPAFASDT 1153

RESULT 4
 A:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 02-Aug-2002
 C:Accession: A55624
 R:Yin, W.; Smiley, R.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez
 J. Biol. Chem. 270, 1798-1806, 1995
 A:Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin
 A:Reference number: A55624; MUID:95130561; PMID:7829516
 A:Accession: A55624
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2871 <YIN>
 A:Cross-references: GR:L29454; NID:9575509; PIDN:AAA56840.1; PID:9575510
 C:Genetics:
 A:Gene: Fbn-1
 C:Superfamily: fibrillin 1; EGF homology
 F:1201-1236/Domain: EGF homology <EGF>

Query Match 12.1%; Score 398.5; DB 2; Length 2871;
 Best local similarity 31.7%; Pred. No. 2.4e-14;
 Matches 104; Conservative 33; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRVG-----GRIDCGWQWARGSQGCPFYVLRRIARI-----RCOLKAVQCPKCKIG 84
 Db 1123 LCRGGVCLNTEGYSRC-----KCPYHQIAINISACIDINNECELSA-----HICPHG 1169
 QY 85 EC-----IGPNKCKCHPGYAGKT-----TCIOVLNEGLKPRCKHRCMNTYGSYKCYCLNGYM 137
 Db 1170 RCYNLIGKYCACNPGYHSTPDLFLCVDI-DEGSIHNGGCTCTNSGSEYSCOPGFA 1228
 QY 138 LMPD-GSCSSALTC--SMANCOYG-CDVVKGQIRKCCQPSGIGLADPGRCTCVW-----187
 Db 1229 LMPDQRSCDTIDECEDNPNICDGGCTNIPGKYKCLC-YDGFMASSDMKTCVDVNSCDLN 1287
 QY 188 -----DECATGRASCPREFRCQCVNTEGYSYI 211
 Db 1288 PNIICLSCTCHTKGSPICHCMDGYSCKKGTCTDINKEEIGAHNCDRAVCINTASSPK 1347
 QY 212 CKCHKGHDLIMYIGKGYOCHDIDECISLGOYCCSFARCYNVKSGYKCKKPGYCGDGLTCV 271
 Db 1348 CSCSPG---WIGDGKICKTDLDECSNCTUMCSQADCKNTMGSYRCLCKEYGTGDTCT 1403
 QY 272 YIPKVMIEPSCPIHVPKGNCTILKGDIG 299
 Db 1404 DLD-----ECSENLNL-CGNGCCLNAPCG 1426

R:Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.
 Eur. J. Biochem. 240, 427-434, 1996
 A:Title: Different susceptibilities of fibrulin-1 and fibrulin-2 to cleavage by matrix
 A:Reference number: S74094; MUID:96439073; PMID:8841408
 A:Accession: S74095
 A:Molecule type: protein
 A:Residues: 236-238, X*, 240-247, 260-275, 336-344, Y*, 446-461, 405, 426, 566, 568, YPM*, 569
 C:Superfamily: fibrulin-2; EGF homology
 C:Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer
 F:942-978/Domain: EGF homology <EGF>

Query Match 12.2%; Score 402; DB 2; Length 1221;
 Best local similarity 36.6%; Pred. No. 7.1e-15;
 Matches 93; Conservative 29; Mismatches 92; Indels 40; Gaps 14;

QY 80 RCKIGE-CI---GPNKCKCHPGYA---GKTCIOVLNEGLKPRCKHRCMNTYGSYK 130
 Db 905 RCGRGOLCYNLPGSYKCKCKPGQFQFATQFCTDV-NRWSPSGHICQHTENTETSYRC 963
 QY 131 YCINLYMIMPDS-CSSALTCSSMANCOYGCDVVKGQIRKCCQPSGIGLADPGRCTCVW 189
 Db 964 SCANGFLAADCCKICEDVNECETBRCSECCANTYGSYCYC-RCGYOLAEKGLTCTDDE 1022
 QY 190 CATGRASCPREFRCQCVNTEGYSYICKC-HKGFDMYIGKGYOCHDIDECISLGOYCCSFAR 248
 Db 1023 CAQAGCIICTFE-CVNVPGSYCACPEGQYTMNANG-RSCCKIDDECALGTHNCSSEATC 1079
 QY 249 YNVGSGYK---CKEGY-----QSDGLTCVYIPKVMIEPSC-----PIH 285
 Db 1080 HNIQGSFCLRFCDPNVYVKSQIKCERPTCDITFCQTSIPARITHYGLNFVGLLVIAH 1119
 QY 286 VPK-GNCTILKGIPT 298
 Db 1140 IFRIGPAPAFASDT 1153

RESULT 4
 A:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 02-Aug-2002
 C:Accession: A55624
 R:Yin, W.; Smiley, R.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez
 J. Biol. Chem. 270, 1798-1806, 1995
 A:Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin
 A:Reference number: A55624; MUID:95130561; PMID:7829516
 A:Accession: A55624
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2871 <YIN>
 A:Cross-references: GR:L29454; NID:9575509; PIDN:AAA56840.1; PID:9575510
 C:Genetics:
 A:Gene: Fbn-1
 C:Superfamily: fibrillin 1; EGF homology
 F:1201-1236/Domain: EGF homology <EGF>

Query Match 12.1%; Score 398.5; DB 2; Length 2871;
 Best local similarity 31.7%; Pred. No. 2.4e-14;
 Matches 104; Conservative 33; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRVG-----GRIDCGWQWARGSQGCPFYVLRRIARI-----RCOLKAVQCPKCKIG 84
 Db 1123 LCRGGVCLNTEGYSRC-----KCPYHQIAINISACIDINNECELSA-----HICPHG 1169
 QY 85 EC-----IGPNKCKCHPGYAGKT-----TCIOVLNEGLKPRCKHRCMNTYGSYKCYCLNGYM 137
 Db 1170 RCYNLIGKYCACNPGYHSTPDLFLCVDI-DEGSIHNGGCTCTNSGSEYSCOPGFA 1228
 QY 138 LMPD-GSCSSALTC--SMANCOYG-CDVVKGQIRKCCQPSGIGLADPGRCTCVW-----187
 Db 1229 LMPDQRSCDTIDECEDNPNICDGGCTNIPGKYKCLC-YDGFMASSDMKTCVDVNSCDLN 1287
 QY 188 -----DECATGRASCPREFRCQCVNTEGYSYI 211
 Db 1288 PNIICLSCTCHTKGSPICHCMDGYSCKKGTCTDINKEEIGAHNCDRAVCINTASSPK 1347
 QY 212 CKCHKGHDLIMYIGKGYOCHDIDECISLGOYCCSFARCYNVKSGYKCKKPGYCGDGLTCV 271
 Db 1348 CSCSPG---WIGDGKICKTDLDECSNCTUMCSQADCKNTMGSYRCLCKEYGTGDTCT 1403
 QY 272 YIPKVMIEPSCPIHVPKGNCTILKGDIG 299
 Db 1404 DLD-----ECSENLNL-CGNGCCLNAPCG 1426

Db 1288 PNILSGTGTGSGFICHDGYSKKGKGTCTDINECEIGAHNCGRHAVCTNTAGSFK 1347
 :||| | :||| | :||| | :||| | :||| |

QY 212 CKCHGFDLMYIGKYQCHDIDECISLQYQCSFARCYNVRGSKCKCKGQGGDLTCV 271
 :||| | :||| | :||| | :||| | :||| |

Db 1348 CSCSPG---WIGDGKICTDLDECSTNGTHMCSQHADCKNTMSYRCCLKDGYTGDSFTCT 1403
 :||| | :||| | :||| | :||| | :||| |

QY 272 YTPKVAIEPSGPIHPKNGTILKGDGTG 299
 :||| | :||| | :||| | :||| | :||| |

Db 1404 DLD---ECSENLNLCGNGCQCLNAPGG 1426
 :||| | :||| | :||| | :||| | :||| |

RESULT 5

A54105

fibrillin-2 precursor - human

C:Species: Homo sapiens (man)

C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Aug-2002

C:Accession: A54105; S17063; S31101

R:Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, E.C.; Sanguinetti, C.; Bonadio, J.; Mecham,

J. Cell Biol. 124, 855-863, 1994

A:Title: Structure and expression of fibrillin-2, a novel microfibrillar component prefe

A:Reference number: A54105; MUID:94165150; PMID:8120105

A:Accession: A54105

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-2918 <ZHA>

A:Cross-references: GB:003272

R:Lee, H.; Godfrey, M.; Vitale, E.; Hori, H.; Mattel, M.G.; Sarfarazi, M.; Tsipouras, P.

Nature 352, 330-334, 1991

A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differe

A:Reference number: S17062; MUID:91304567; PMID:1852206

A:Accession: S17063

A:Molecule type: mRNA

A:Residues: 752-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928 <LEE>

A:Cross-references: EMBL:X62009

R:Milewicz, D.M.

submitted to the EMBL Data Library, December 1992

A:Reference number: S31101

A:Molecule type: mRNA

A:Residues: 752-1407,'R',1409-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928

A:Cross-references: EMBL:X62009

C:Genetics:

A:Gene: GDB:FBN2

A:Cross-references: GDB:128122; OMIM:121050

A:Map position: 5q23-5q31

C:Superfamily: fibrillin 1; EGF homology

C:Keywords: extracellular protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:10-2918/Product: fibrillin-2 #status predicted <MAT>

F:1245-1280/Domain: EGF homology <EGF1>

F:1970-2013/Domain: EGF homology <EGF>

Query Match 12.1%; Score 397.5; DB 2; Length 2918;

Best Local Similarity 35.0%; Pred. No. 2.7e-14;

Matches 84; Conservative 31; Mismatches 72; Indels 53; Gaps 9;

QY 81 CKHCEC---IGPNKCKCHPGYAG----KTCIQVLNECGLKPRPKHRCMNTYGSYKCYCL 133
 :||| | :||| | :||| | :||| | :||| |

Db 1210 CRNGKCVNMIGTYQCSNPGYATPDROGCTDI-DECMIMNGGCTDCTNSGSEYECSCS 1268
 :||| | :||| | :||| | :||| | :||| |

QY 134 NGYMLMPDG-SCSSALTC--SWANCQYG-CDVVKQIRQCPSPGIQLAPDGRTCVDVDE 189
 :||| | :||| | :||| | :||| | :||| |

Db 1269 EGYALMPDGRSCADIDECENNPDIICUGGQCTNIPGKYRCIJC-YDGFMA5MDMKTKCIDVNE 1327
 :||| | :||| | :||| | :||| | :||| |

QY 190 CATGRASCPFRQCNTVTFSGYICKCKHKGFDLM----- 221
 :||| | :||| | :||| | :||| | :||| |

Db 1328 CDLSNMC-MFGECENTKGSFICHQOLGYSVKKGTTGCTDVEDCEETGAINCDMHASCLNI 1386
 :||| | :||| | :||| | :||| | :||| |

QY 222 -----YIGGYQCHDIDECISLQYQCSFARCYNVRGSKCKCKGQGGDLTC 270
 :||| | :||| | :||| | :||| | :||| |

Db 1387 PGSEKSCREGWLGNGIKCIDLDECSTNGTHMCSQHADCKNTMSYRCCLKDGYTGDSFTCT 1446
 :||| | :||| | :||| | :||| | :||| |

RESULT 6

A57278

fibrillin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 02-Aug-2002

C:Accession: A57278

R:Zhang, H.; Hu, W.; Ramirez, F.

J. Cell Biol. 129, 1165-1176, 1995

A:Title: Developmental expression of fibrillin genes suggests heterogeneity of extrac

A:Reference number: A57278; MUID:95263670; PMID:7744963

A:Accession: A57278

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2907 <ZHA>

A:Cross-references: GR:139790; NID:g762830; PIDN:AAA74908.1; PID:g762831

C:Superfamily: fibrillin 1; EGF homology

F:1239-1274/Domain: EGF homology <EGF1>

F:2488-2523/Domain: EGF homology <EGF>

Query Match 12.1%; Score 397; DB 2; Length 2907;

Best Local Similarity 33.1%; Pred. No. 2.9e-14;

Matches 79; Conservative 33; Mismatches 74; Indels 16; Gaps 9;

QY 81 CKHCEC---IGPNKCKCHPGYAG----KTCIQVLNECGLKPRPKHRCMNTYGSYKCYCL 133
 :||| | :||| | :||| | :||| | :||| |

Db 1204 CRNGKCVNMIGTYQCSNPGYATPDROGCTDI-DECMIMNGGCTDCTNSGSEYECSCS 1262
 :||| | :||| | :||| | :||| | :||| |

QY 134 NGYMLMPDG-SCSSALTC--SWANCQYG-CDVVKQIRQCPSPGIQLAPDGRTCVDVDE 189
 :||| | :||| | :||| | :||| | :||| |

Db 1263 EGYALMPDGRSCADIDECENNPDIICUGGQCTNIPGKYRCIJC-YDGFMA5MDMKTKCIDVNE 1321
 :||| | :||| | :||| | :||| | :||| |

QY 190 CATGRASCPFRQCNTVTFSGYICKCKHKGFDLMYIGKYQCHDIDECISLQYQCSFARCY 249
 :||| | :||| | :||| | :||| | :||| |

Db 1322 CDLSNMC-MFGECENTKGSFICHQOLGYSVK--KGTTGCTDVEDCEETGAINCDMHASCL 1378
 :||| | :||| | :||| | :||| | :||| |

QY 250 NVRGSKCKCKEGYOGDGLTCV 271
 :||| | :||| | :||| | :||| | :||| |

Db 1379 NVPGSEKSCREGWVGNGIKC: 1400
 :||| | :||| | :||| | :||| | :||| |

RESULT 7

A47221

fibrillin 1 precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002

C:Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R:Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomics 17, 476-484, 1993

A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain stru

A:Reference number: A47221; MUID:94010947; PMID:7691719

A:Accession: A47221

A:Molecule type: mRNA

A:Residues: 1-337,'T',339-1029 <COR>

A:Cross-references: GB:X63556

R:Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Fanfili, T.; Bo

Hum. Mol. Genet. 2, 961-968, 1993

A:Title: Genomic organization of the sequence coding for fibrillin, the defective gen

A:Reference number: I54355; MUID:93372860; PMID:8364578

A:Accession: I54355

A:Status: preliminary; translated from GB/EMBL/DDDBJ

A:Molecule type: mRNA

A:Residues: 132-3002 <PER>

A:Cross-references: GR:133923; NID:g306745; PIDN:AAH02016.1; PID:g306746

R:Maslen, C.L.; Corson, G.M.; Maddox, H.K.; Glanville, R.W.; Sakai, L.Y.

Nature 352, 334-337, 1991

A:Title: Partial sequence of a candidate gene for the Marfan syndrome.

A:Reference number: S17064; MUID:91304568; PMID:1852207

A:Accession: S17064

A:Molecule type: mRNA

A:Residues: 1030-3002 <MAS>

A:Cross-references: EMBL:X63556

R:Dietz, H.C.; Valle, D.; Francomano, G.A.; Kendzior, R.J.

C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 02 Aug 2002
C:Accession: A51184; Y08744
R:Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.L.
Genomics 22, 425-430, 1994
A:Title: Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping of the
A:Reference number: A55184; MUID:95104855; PMID:7806240
A:Accession: A55184
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1184 <ZHA>
A:Cross-references: GB:X82494; NID:4575232; PION:OAA57876.1; PII:q575244
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z16471
A:Accession: Y08744
A:Molecule type: mRNA
A:Residues: 656-719; QDEELMGAGHDCSRQFCVNTLGSFYCVNITVLCAQGYILNLIHKKVVD; /20 85A, 71', 85A
A:Cross-references: EMBL:AL050095
A:Experimental source: adult uterus; clone DKFZp586A1519
C:Genetics:
A:Gene: GDB:FBLN2
A:Cross-references: GDB:293037; OMIM:135821
A:Map position: 3p25-3p24
A:Note: DKFZp586A1519.1
C:Superfamily: fibulin-2; EGF homology
C:Keywords: alternative splicing; extracellular matrix
F:1-27/Domain: signal sequence #status predicted -SIG>
F:28-1184/Product: Fibulin-2 protein #status predicted -MAP>
F:905-941/Domain: EGF homology <EGF>

[illegible]

RESULT 9
 T13954
 MEGF6 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21 Jul 2000
 C:Accession: T13954
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Seki, N.; Ohata, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; M01D:98360089; PMID:9694040
 A:Accession: T13954
 A:Status: Preliminary; translated from CD/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1574 -NAK>
 A:Cross-references: NID:q1449294; PIDN:RAA12462.1; PID:q1449294
 A:Experimental source: strain Sprague Dawley; brain
 C:Genetics:


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A:Accession: A32826
A:Molecule type: Protein
A:Residues: 30-35, 'SX', 38-40, 'SH', 43-44 <ARG>
C:Genetics:
A:Gene: GDB:FBLN1: FBLN
A:Cross-references: GDB:278285; OMIM:135820
A:Map position: 22q13.3-22q13.3
A:Superfamily: fibulin-1; EGF homology
C:Keywords: alternative splicing; glycoprotein
F:1-29/Domain: signal sequence *status predicted <SIG>
F:10-683/Product: fibulin 1 splice form C *status predicted <SIG>
F:180-214/Domain: EGF homology <EGF>
F:485-523/Domain: EGF homology <EGF>
F:98-535/Binding site: carbohydrate (Asn) (covalent) *status predicted

Query Match 10.3%; Score 340; DB 2; Length 683;
Best Local Similarity 31.2%; Pred. No. 1,1e-11;
Matches 91; Conservative 47; Mismatches 108; Indels 60; Gaps 17;

QY 31 SSIGLCHYGRIDCCWQWQSWCOC-----QPFYVLRKRIAR 68
DB 281 NTLGSPRCRKLQKSGFIQDALGNCIDNECLISAPCPIGHITCINTGSSYTCCKNVPN 340
QY 69 -----IRCOLKAVQCP---RCKHG-ECI---GPNKCKCHPY---AGKTCIQV 106
DB 141 CGRCYHLEERTKCVDDVECAPAPKPCGKGRHCNVNSPGSPRCECKTGYYPFXGISRMCVDV 400
QY 107 LNEGLKP-BPCKHGMNTYSKYCYCLNGYMLMPDG-SCSSALTCSMANQYQCTVVKG 164
DB 401 -NRCORYPGRLGCHKCENTLGSVGCSPGFRISVGRSCEDINPKCSSSCSPCKANVYG 459
QY 165 QIRCOCHSPGILQAP-DGRTCTVVDDECA---TGRASCPRRPQCVNTPGSYICKK-HKGFDL 220
DB 460 SYQCYC-RRGYQLSDVDGVTCEIDECALPTGGHICS--YRCINIPGSPFCSSGYRL 516
QY 221 MYTGKYOCHDIDRCSLQYQCSFARCYNVNRSYKC---KCKHGYGDCGLT-CVYIP 274
DB 517 APNG--NRCQIDICVTVGHNCISINFTCFNLOGAFCRLAECPEVNRSAATRCERLP 572

RESULT 13
#36346
fibulin 1 precursor, splice form H - human
C:Species: Homo sapiens (man)
C:Date: 19-Apr-1991 *sequence_revision 19-Apr-1991 *text_change 02-Aug-2002
C:Accession: #36346
F:Acquires: W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
J. Cell Biol. 111, 3155-3164, 1990
A:Title: Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain
A:Reference number: A36446; MUID:91100426; PMID:2269669
A:Molecule type: mRNA
A:Residues: 1-601 <ARG>
A:Cross-references: GDB:278285; OMIM:135820
C:Genetics:
A:Gene: GDB:FBLN1: FBLN
A:Cross-references: GDB:278285; OMIM:135820
A:Map position: 22q13.3-22q13.3
A:Superfamily: fibulin-1; EGF homology
C:Keywords: alternative splicing
F:180-214/Domain: EGF homology <EGF>
F:485-523/Domain: EGF homology <EGF>

Query Match 10.3%; Score 338; DB 2; Length 601;
Best Local Similarity 31.7%; Pred. No. 1.2e-11;
Matches 83; Conservative 45; Mismatches 86; Indels 58; Gaps 15;

QY 56 QPFYVLRKRIARICQLKAVQCP---RCKHGRICIGNKC----- 92
DB 273 CLPQICNTLGSFRCPKLOCKSGFIQDALGNCIDNECLISAPCPIGHITCINTGSSY 332
QY 93 -----KCHPCY---AGKTCIQVLRKRIARICQLKAVQCP---KHKCMNTYGSYKCYCLNGYMLM 139

A:Accession: A32826
A:Molecule type: Protein
A:Residues: 30-35, 'SX', 38-40, 'SH', 43-44 <ARG>
C:Genetics:
A:Gene: GDB:FBLN1: FBLN
A:Cross-references: GDB:278285; OMIM:135820
A:Map position: 22q13.3-22q13.3
A:Superfamily: fibulin-1; EGF homology
C:Keywords: alternative splicing
F:180-214/Domain: EGF homology <EGF>
F:485-523/Domain: EGF homology <EGF>

Query Match 10.2%; Score 334.5; DB 2; Length 685;
Best Local Similarity 28.8%; Pred. No. 2.2e-11;
Matches 88; Conservative 32; Mismatches 93; Indels 94; Gaps 15;

QY 56 QPFYVLRKRIARICQLKAVQCP----- 78
DB 275 CPPDFICQNTLGSFRCPKLOCKSGFIQDALGNCIDNECLISAPCPIGHITCINTGSSY 334
QY 79 -----PRCKHG-----RCKHGRICIGNKC----- 98
DB 335 TCCKNVPNCGRYILNEEGTRCVIVDECAAPAEPCGKGRHCNVNSPGSPRCECKHGYFEG 394
QY 99 AGKTCIQVLRKRIARICQLKAVQCP---RCKHGRICIGNKC----- 196
DB 395 ISPTCVDT-NRCORYPGRLGCHKCENTLGSVGCSPGFRISVGRSCEDINPKCSSSCSPCKANVYG 459
QY 157 YGCDVVKGQIRCOCHSPGILQAP-DGRTCTVVDDECA---TGRASCPRRPQCVNTPGSYICKK 214
DB 454 QECANVYGSYQCYC-RRGYQLSDVDGVTCEIDECALPTGGHICS--YRCINIPGSPFCSS 510
QY 214 C-HKGFDLMYIGKYOCHDIDRCSLQYQCSFARCYNVNRSYKC---KCKHGRICIGNKC----- 269
DB 511 CPSSGYKLAPNG--RNCQIDICVTVGHNCISINFTCFNLOGAFCRLAECPEVNRSAAT 568
QY 270 -CVYIP 274
DB 569 RCARLP 574

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RESULTS 15

S34968
fibulin, splice form D precursor - mouse
N:Alternate names: basement-membrane protein BM-90; calcium-binding protein BM-90
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C:Accession: S34968; S36441; S13814
R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A:Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A:Reference number: S34968; MUID:93358897; PMID:8354280
A:Accession: S34968
A:Molecule type: mRNA
A:Residues: 1-705 <PAN>
R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A:Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dep
A:Reference number: S36440
A:Accession: S36441
A:Molecule type: mRNA
A:Residues: 1-39, 'P', 41-705 <PAN>
C:Cross-references: EMBL:X70854; NID:q396820; PIDN:CAA50207.1; PID:q396821
A:Experimental source: cell-line F9 teratocarcinoma
R:Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R.
Eur. J. Biochem. 193, 651-659, 1990
A:Title: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90) shared
A:Reference number: S13814; MUID:91065369; PMID:2249686
A:Accession: S13814
A:Molecule type: protein
A:Residues: 28;31-49, 'X', 51-53; 'XX', 110-117;231-240, 'X', 242-243;339-362, 'S', 364-387;434-
C:Superfamily: fibulin-1; EGF homology
C:Keywords: alternative splicing; basement membrane; calcium binding; extracellular mat
F:1-29/domain: signal sequence #status predicted <SIG>
F:30-705/Product: fibulin, splice form D #status predicted <MAT>
F:98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 332; DB 2; Length 705;
Best Local Similarity 30.9%; Pred. No. 3.1e-11;
Matches 82; Conservative 36; Mismatches 83; Indels 64; Gaps 15;

QY 56 CQPEYVLRQRIARICQLKAVQCP---RCKHGECIGPNKC----- 92
DB 275 CPPDFICQNTLGSFRCPKLPCKSGFIQDALGNCIDINHCISISAPCPVQCICINTFGSY 334
QY 93 -----KCHPGY----ACKTCIQVINECGLKPRPC--KHRCMNTYGSYKCYCLNGYMLM 139
DB 335 TCQKNVPNCGRGYHNEEGTRCDV-DECAPPAEPGKGHGLNSPGSFRCEKAGFYF- 392
QY 140 PDGSCSALITCSMAN-----COYGDVVYKQIHCQCPSPGIQLADPGHTCVDVDFC 190
DB 393 -DG---ISRTCVDINPCQRYHPGRLCGHKCENTPGSPHCSC-SAGFRLSVDGKSCEDVNEC 447
QY 191 ATGRASCPREFRCVNTFGSYICKKHGKEDLMVIGKYGQCHIDIEGSL--GOYQCSFARC 248
DB 448 ----LNSPSCQECANVYGSYQCYCRGYQLSDVDG-VTCEDIDECALPTCGHICS--YRC 500
QY 249 YNVKSGYKCKC-KEGYQ--CDGITC 270
DB 501 INIPGSFQSCSPSSGYRLAPNGRNC 525

Search completed: April 23, 2003, 13:03:43
Job time : 33 secs

